AMENDMENTS TO THE SPECIFICATION

Please amend the title as follows:

~~SECRETED AND TRANSMEMBRANE~~ POLYPEPTIDES ~~AND NUCLEIC ACIDS ENCODING THE SAME~~ THAT INDUCE CELL PROLIFERATION

Please amend the paragraph starting on line 1 of page 75 as follows:

--Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., <u>Nucleic Acids Res.</u> 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from ~~http://www.ncbi.nlm.nih.gov~~<u>the National Institutes of Health website</u> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

Please amend the paragraph starting on line 22 of page 77 as follows:

--Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., <u>Nucleic Acids Res.</u> 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from ~~http://www.ncbi.nlm.nih.gov~~<u>the National Institutes of Health website</u> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--